

# SEQUENCE LISTING

<110> Haley, Dana A  
Boyle, Bryan J  
Ho, Alice S  
Arterburn, Matthew C  
Tang, Y. Tom  
Tillinghast, John S  
Sinku, Ankura  
Liu, Chenghua  
Drmanac, Radoje T

<120> METHODS AND MATERIALS RELATING TO NOVEL  
PROTHROMBINASE-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

<130> HYS-14

<140> Not Yet Assigned

<141> 2000-06-17

<150> 09/552,317

<151> 2000-04-25

<150> 09/488,725

<151> 2000-01-21

<160> 9

<170> PatentIn Ver. 2.1

<210> 1

<211> 725

<212> DNA

<213> Homo sapiens

<400> 1

```
ctgatcttaa ggataccatt ggctctgtca ccaaaacacc gagtggttta tacataattc 60
accagaagg atctagctac ccatctgagg taatgtgtga catggattac agaggaggtg 120
gatggactgt gatacagaaa agaattgatg ggataattga tttccagagg ttgtggtgtg 180
attatctgga tggatttgga gatcttctag gagaattttg gctaggactg aaaaagattt 240
tttatatagt aaatcacaaa aataaccagtt ttatgctgta tgtggctttg gaatctgaag 300
atgacactct tgcttatgca tcatatgata atttttggct agaggatgaa acgagatttt 360
ttaaaatgca cttaggacgg tattcaggaa atgctggtga tgcattccgg ggtctcaaaa 420
aagaagataa tcaaaatgca atgcctttta gcacatcaga tgttgataat gatgggtgtc 480
gccctgcatg cctggtcaat ggtcaatctg tgaagagctg gagtcacctt cataacaaga 540
ccgggctgtg gtttaacgag tgtgggctaa ccaatctaaa tggcattcat cacttctctt 600
ggaaaatggc ttgcaactgg aattcaatgg gggcacgtgg gaccacaaac cacttaacct 660
gtccaaggaa ttaaactctg gttccactgg aaaattagga agaaatgtgc caattccata 720
```

09596196.06.17.00

T, 1160

ttttt

725

<210> 2

<211> 1069

<212> DNA

<213> Homo sapiens

<400> 2

ctgatcttaa ggataaccatt ggctctgtca ccaaaacacc gagtggttta tacataattc 60  
accagaagg atctagctac ccatttgagg taatgtgtga catggattac agaggagggtg 120  
gatggactgt gatacagaaa agaattgatg ggataattga tttccagagg ttgtgggtgtg 180  
attatctgga tggatttgga gatcttctag gagaattttg gctaggactg aaaaagattt 240  
tttatatagt aaatcagaaa aataccagtt ttatgctgta tgtggctttg gaatctgaag 300  
atgacactct tgcttatgca tcatatgata atttttggct agaggatgaa acgagatttt 360  
ttaaagtgc cttaggacgg tattcaggaa atgctgggtga tgcattccgg ggtctcaaaa 420  
aagaagataa tcaaaatgca atgcctttta gcacatcaga tgttgataat gatgggtgtc 480  
gccctgcatg cctgggtcaat ggtcagtctg tgaagagctg cagtcacctc cataacaaga 540  
ccggctggtg gtttaacgag tgtgggtctag caaatctaaa tggcattcat cacttctctg 600  
gaaaattgct tgcaactgga attcaatggg gcacgtggac caaaaacaac tcacctgtca 660  
agattaaatc tgtttcaatg aaaattagaa gaatgtacaa tccatatttt aaataatctc 720  
atttaacatt gtaatgcaag ttctacaatg ataatatatt aaagattttt aaaagtttat 780  
cttttcactt agtgtttcaa acatattagg caaaatttaa ctgtagatgg cathtagatg 840  
ttatgagttt aattagaaaa cttcaatttt gtagtattct ataaaagaaa acatggctta 900  
ttgtatgttt ttacttctga ctatattaac aatatacaat gaaatttggt tcaagtgaac 960  
tacaacttgt cttcctaaaa tttatagtga ttttaaagga ttttgccttt tctttgaagc 1020  
atttttaaac cataatatgt tgtaaggaaa attgaaggga atattttac 1069

<210> 3

<211> 2013

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1167)

<400> 3

atg atg tct cca tcc caa gcc tca ctc tta ttc tta aat gta tgt att 48  
Met Met Ser Pro Ser Gln Ala Ser Leu Leu Phe Leu Asn Val Cys Ile  
1 5 10 15  
  
ttt att tgt gga gaa gtt gta caa ggt aac tgt gta cat cat tct acg 96  
Phe Ile Cys Gly Glu Val Val Gln Gly Asn Cys Val His His Ser Thr  
20 25 30  
  
gac tct tca gta gtt aac att gta gaa gat gga tct aat gca aaa gat 144

Asp	Ser	Ser	Val	Val	Asn	Ile	Val	Glu	Asp	Gly	Ser	Asn	Ala	Lys	Asp	
		35					40					45				
gaa	agt	aaa	agt	aat	gat	act	gtt	tgt	aag	gaa	gac	tgt	gag	gaa	tca	192
Glu	Ser	Lys	Ser	Asn	Asp	Thr	Val	Cys	Lys	Glu	Asp	Cys	Glu	Glu	Ser	
		50				55					60					
tgt	gat	gtt	aaa	act	aaa	att	aca	cga	gaa	gaa	aaa	cat	ttc	atg	tgt	240
Cys	Asp	Val	Lys	Thr	Lys	Ile	Thr	Arg	Glu	Glu	Lys	His	Phe	Met	Cys	
		65			70				75						80	
aga	aat	ttg	caa	aat	tct	att	gtt	tcc	tac	aca	aga	agt	acc	aaa	aaa	288
Arg	Asn	Leu	Gln	Asn	Ser	Ile	Val	Ser	Tyr	Thr	Arg	Ser	Thr	Lys	Lys	
				85				90						95		
cta	cta	agg	aat	atg	atg	gat	gag	caa	caa	gct	tcc	ttg	gat	tat	tta	336
Leu	Leu	Arg	Asn	Met	Met	Asp	Glu	Gln	Gln	Ala	Ser	Leu	Asp	Tyr	Leu	
			100				105					110				
tct	aat	cag	gtt	aac	gag	ctc	atg	aat	aga	gtt	ctc	ctt	ttg	act	aca	384
Ser	Asn	Gln	Val	Asn	Glu	Leu	Met	Asn	Arg	Val	Leu	Leu	Leu	Thr	Thr	
		115				120					125					
gaa	gtt	ttt	aga	aaa	cag	ctg	gat	cct	ttt	cct	cac	aga	cct	gtt	cag	432
Glu	Val	Phe	Arg	Lys	Gln	Leu	Asp	Pro	Phe	Pro	His	Arg	Pro	Val	Gln	
		130			135					140						
tca	cat	ggg	tta	gat	tgc	act	gat	att	aag	gat	acc	att	ggc	tct	gtc	480
Ser	His	Gly	Leu	Asp	Cys	Thr	Asp	Ile	Lys	Asp	Thr	Ile	Gly	Ser	Val	
		145			150				155						160	
acc	aaa	aca	ccg	agt	ggg	tta	tac	ata	att	cac	cca	gaa	gga	tct	agc	528
Thr	Lys	Thr	Pro	Ser	Gly	Leu	Tyr	Ile	Ile	His	Pro	Glu	Gly	Ser	Ser	
			165					170						175		
tac	cca	ttt	gag	gta	atg	tgt	gac	atg	gat	tac	aga	gga	ggg	gga	tgg	576
Tyr	Pro	Phe	Glu	Val	Met	Cys	Asp	Met	Asp	Tyr	Arg	Gly	Gly	Gly	Trp	
			180				185						190			
act	gtg	ata	cag	aaa	aga	att	gat	ggg	ata	att	gat	ttc	cag	agg	ttg	624
Thr	Val	Ile	Gln	Lys	Arg	Ile	Asp	Gly	Ile	Ile	Asp	Phe	Gln	Arg	Leu	
		195				200					205					
tgg	tgt	gat	tat	ctg	gat	gga	ttt	gga	gat	ctt	cta	gga	gaa	ttt	tgg	672
Trp	Cys	Asp	Tyr	Leu	Asp	Gly	Phe	Gly	Asp	Leu	Leu	Gly	Glu	Phe	Trp	
		210				215				220						
cta	gga	ctg	aaa	aag	att	ttt	tat	ata	gta	aat	cag	aaa	aat	acc	agt	720

Leu Gly Leu Lys Lys Ile Phe Tyr Ile Val Asn Gln Lys Asn Thr Ser  
 225 230 235 240

ttt atg ctg tat gtg gct ttg gaa tct gaa gat gac act ctt gct tat 768  
 Phe Met Leu Tyr Val Ala Leu Glu Ser Glu Asp Asp Thr Leu Ala Tyr  
 245 250 255

gca tca tat gat aat ttt tgg cta gag gat gaa acg aga ttt ttt aaa 816  
 Ala Ser Tyr Asp Asn Phe Trp Leu Glu Asp Glu Thr Arg Phe Phe Lys  
 260 265 270

atg cac tta gga cgg tat tca gga aat gct ggt gat gca ttc cgg ggt 864  
 Met His Leu Gly Arg Tyr Ser Gly Asn Ala Gly Asp Ala Phe Arg Gly  
 275 280 285

ctc aaa aaa gaa gat aat caa aat gca atg cct ttt agc aca tca gat 912  
 Leu Lys Lys Glu Asp Asn Gln Asn Ala Met Pro Phe Ser Thr Ser Asp  
 290 295 300

gtt gat aat gat ggg tgt cgc cct gca tgc ctg gtc aat ggt cag tct 960  
 Val Asp Asn Asp Gly Cys Arg Pro Ala Cys Leu Val Asn Gly Gln Ser  
 305 310 315 320

gtg aag agc tgc agt cac ctc cat aac aag acc ggc tgg tgg ttt aac 1008  
 Val Lys Ser Cys Ser His Leu His Asn Lys Thr Gly Trp Trp Phe Asn  
 325 330 335

gag tgt ggt cta gca aat cta aat ggc att cat cac ttc tct gga aaa 1056  
 Glu Cys Gly Leu Ala Asn Leu Asn Gly Ile His His Phe Ser Gly Lys  
 340 345 350

ttg ctt gca act gga att caa tgg ggc acg tgg acc aaa aac aac tca 1104  
 Leu Leu Ala Thr Gly Ile Gln Trp Gly Thr Trp Thr Lys Asn Asn Ser  
 355 360 365

cct gtc aag att aaa tct gtt tca atg aaa att aga aga atg tac aat 1152  
 Pro Val Lys Ile Lys Ser Val Ser Met Lys Ile Arg Arg Met Tyr Asn  
 370 375 380

cca tat ttt aaa taa tctcatttaa cattgtaatg caagttctac aatgataata 1207  
 Pro Tyr Phe Lys  
 385

tattaaagat ttttaaaagt ttatcttttc acttagtggt tcaaacatat taggcaaaat 1267

ttaactgtag atggcattta gatgttatga gtttaattag aaaacttcaa ttttgtagta 1327

ttctataaaa gaaaacatgg cttattgtat gtttttactt ctgactatat taacaatata 1387

caatgaaatt tgtttcaagt gaactacaac ttgtcttcct aaaatttata gtgattttta 1447  
 aggattttgc cttttctttg aagcattttt aaaccataat atgttgtaag gaaaattgaa 1507  
 gggaatattt tacttatttt tatactttat atgattatat aatctacaga taatttctac 1567  
 tgaagacagt tacaataaat aactttatgc agattaatat ataagctaca catgatgtaa 1627  
 aaaccttact atttctaggt gatgccatac cattttaaaa gtagtaagag tttgctgccc 1687  
 aaatagtttt tcttgttttc atatctaatac atggttaact attttgttat tgtttgtaat 1747  
 aaatatatgt acttttatat cctgaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1807  
 aaaaaaaagg ggcgcccctt taatttaaag gggcccttta aaccccggtt aaaccccggt 1867  
 aggggggcttt tatagggccc ccccttggtg tgtgcccccc ccccggggtt ttttttgacg 1927  
 ggggggggggc cccccccact tttttttttt taaaaaaaag agaaaattcc ccccttttgt 1987  
 gggaagggggg gttttttttt ttggggg 2013

<210> 4  
 <211> 388  
 <212> PRT  
 <213> Homo sapiens

<400> 4  
 Met Met Ser Pro Ser Gln Ala Ser Leu Leu Phe Leu Asn Val Cys Ile  
 1 5 10 15  
 Phe Ile Cys Gly Glu Val Val Gln Gly Asn Cys Val His His Ser Thr  
 20 25 30  
 Asp Ser Ser Val Val Asn Ile Val Glu Asp Gly Ser Asn Ala Lys Asp  
 35 40 45  
 Glu Ser Lys Ser Asn Asp Thr Val Cys Lys Glu Asp Cys Glu Glu Ser  
 50 55 60  
 Cys Asp Val Lys Thr Lys Ile Thr Arg Glu Glu Lys His Phe Met Cys  
 65 70 75 80  
 Arg Asn Leu Gln Asn Ser Ile Val Ser Tyr Thr Arg Ser Thr Lys Lys  
 85 90 95  
 Leu Leu Arg Asn Met Met Asp Glu Gln Gln Ala Ser Leu Asp Tyr Leu  
 100 105 110  
 Ser Asn Gln Val Asn Glu Leu Met Asn Arg Val Leu Leu Thr Thr  
 115 120 125  
 Glu Val Phe Arg Lys Gln Leu Asp Pro Phe Pro His Arg Pro Val Gln  
 130 135 140

09596196 "061700

Ser His Gly Leu Asp Cys Thr Asp Ile Lys Asp Thr Ile Gly Ser Val  
 145 150 155 160  
 Thr Lys Thr Pro Ser Gly Leu Tyr Ile Ile His Pro Glu Gly Ser Ser  
 165 170 175  
 Tyr Pro Phe Glu Val Met Cys Asp Met Asp Tyr Arg Gly Gly Gly Trp  
 180 185 190  
 Thr Val Ile Gln Lys Arg Ile Asp Gly Ile Ile Asp Phe Gln Arg Leu  
 195 200 205  
 Trp Cys Asp Tyr Leu Asp Gly Phe Gly Asp Leu Leu Gly Glu Phe Trp  
 210 215 220  
 Leu Gly Leu Lys Lys Ile Phe Tyr Ile Val Asn Gln Lys Asn Thr Ser  
 225 230 235 240  
 Phe Met Leu Tyr Val Ala Leu Glu Ser Glu Asp Asp Thr Leu Ala Tyr  
 245 250 255  
 Ala Ser Tyr Asp Asn Phe Trp Leu Glu Asp Glu Thr Arg Phe Phe Lys  
 260 265 270  
 Met His Leu Gly Arg Tyr Ser Gly Asn Ala Gly Asp Ala Phe Arg Gly  
 275 280 285  
 Leu Lys Lys Glu Asp Asn Gln Asn Ala Met Pro Phe Ser Thr Ser Asp  
 290 295 300  
 Val Asp Asn Asp Gly Cys Arg Pro Ala Cys Leu Val Asn Gly Gln Ser  
 305 310 315 320  
 Val Lys Ser Cys Ser His Leu His Asn Lys Thr Gly Trp Trp Phe Asn  
 325 330 335  
 Glu Cys Gly Leu Ala Asn Leu Asn Gly Ile His His Phe Ser Gly Lys  
 340 345 350  
 Leu Leu Ala Thr Gly Ile Gln Trp Gly Thr Trp Thr Lys Asn Asn Ser  
 355 360 365  
 Pro Val Lys Ile Lys Ser Val Ser Met Lys Ile Arg Arg Met Tyr Asn  
 370 375 380  
 Pro Tyr Phe Lys  
 385

<210> 5  
 <211> 37  
 <212> PRT  
 <213> Homo sapiens

<400> 5  
 Val Met Cys Asp Met Asp Tyr Arg Gly Gly Gly Trp Thr Asx Ile Gln  
 1 5 10 15

Lys Arg Ile Asp Gly Ile Ile Asp Phe Gln Arg Leu Trp Cys Asp Tyr  
 20 25 30

Leu Asp Gly Phe Gly

<210> 6  
 <211> 30  
 <212> PRT  
 <213> Homo sapiens

<400> 6  
 Cys Ser His Leu His Asn Lys Thr Gly Trp Trp Phe Asn Glu Cys Gly  
           1                  5                  10                  15

Leu Ala Asn Leu Asn Gly Ile His His Phe Ser Gly Lys Leu  
                   20                  25                  30

<210> 7  
 <211> 15  
 <212> PRT  
 <213> Homo sapiens

<400> 7  
 Phe Lys Met His Leu Gly Arg Tyr Ser Gly Asn Ala Gly Asp Ala  
           1                  5                  10                  15

<210> 8  
 <211> 13  
 <212> PRT  
 <213> Homo sapiens

<400> 8  
 Glu Phe Trp Leu Gly Leu Lys Lys Ile Phe Tyr Ile Val  
           1                  5                  10

<210> 9  
 <211> 368  
 <212> PRT  
 <213> Homo sapiens

<400> 9  
 Glu Val Val Gln Gly Asn Cys Val His His Ser Thr Asp Ser Ser Val  
           1                  5                  10                  15

Val Asn Ile Val Glu Asp Gly Ser Asn Ala Lys Asp Glu Ser Lys Ser  
                   20                  25                  30

Asn Asp Thr Val Cys Lys Glu Asp Cys Glu Glu Ser Cys Asp Val Lys  
 35 40 45

Thr Lys Ile Thr Arg Glu Glu Lys His Phe Met Cys Arg Asn Leu Gln  
 50 55 60

Asn Ser Ile Val Ser Tyr Thr Arg Ser Thr Lys Lys Leu Leu Arg Asn  
 65 70 75 80

Met Met Asp Glu Gln Gln Ala Ser Leu Asp Tyr Leu Ser Asn Gln Val  
 85 90 95

Asn Glu Leu Met Asn Arg Val Leu Leu Leu Thr Thr Glu Val Phe Arg  
 100 105 110

Lys Gln Leu Asp Pro Phe Pro His Arg Pro Val Gln Ser His Gly Leu  
 115 120 125

Asp Cys Thr Asp Ile Lys Asp Thr Ile Gly Ser Val Thr Lys Thr Pro  
 130 135 140

Ser Gly Leu Tyr Ile Ile His Pro Glu Gly Ser Ser Tyr Pro Phe Glu  
 145 150 155 160

Val Met Cys Asp Met Asp Tyr Arg Gly Gly Gly Trp Thr Val Ile Gln  
 165 170 175

Lys Arg Ile Asp Gly Ile Ile Asp Phe Gln Arg Leu Trp Cys Asp Tyr  
 180 185 190

Leu Asp Gly Phe Gly Asp Leu Leu Gly Glu Phe Trp Leu Gly Leu Lys  
 195 200 205

Lys Ile Phe Tyr Ile Val Asn Gln Lys Asn Thr Ser Phe Met Leu Tyr  
 210 215 220

Val Ala Leu Glu Ser Glu Asp Asp Thr Leu Ala Tyr Ala Ser Tyr Asp  
 225 230 235 240

Asn Phe Trp Leu Glu Asp Glu Thr Arg Phe Phe Lys Met His Leu Gly  
 245 250 255

Arg Tyr Ser Gly Asn Ala Gly Asp Ala Phe Arg Gly Leu Lys Lys Glu  
 260 265 270

Asp Asn Gln Asn Ala Met Pro Phe Ser Thr Ser Asp Val Asp Asn Asp  
 275 280 285

002790"96T9660



Gly Cys Arg Pro Ala Cys Leu Val Asn Gly Gln Ser Val Lys Ser Cys  
290 295 300

Ser His Leu His Asn Lys Thr Gly Trp Trp Phe Asn Glu Cys Gly Leu  
305 310 315 320

Ala Asn Leu Asn Gly Ile His His Phe Ser Gly Lys Leu Leu Ala Thr  
325 330 335

Gly Ile Gln Trp Gly Thr Trp Thr Lys Asn Asn Ser Pro Val Lys Ile  
340 345 350

Lys Ser Val Ser Met Lys Ile Arg Arg Met Tyr Asn Pro Tyr Phe Lys  
355 360 365